

## SEQUENCE LISTING

<110> BASCH, Ross S.  
ZHANG, Xin-Min

<120> PROTEIN THAT MODULATES THE STABILITY OF TRANSCRIPTIONAL REGULATORY COMPLEXES REGULATING NUCLEAR HORMONE RECEPTOR ACTIVITY, DNA ENCODING SAME, AND ANTIBODIES THERETO

<130> BASCH=1A

<140> NOT YET ASSIGNED

<141> 2001-11-15

<150> 60/248,191

<151> 2000-11-15

<160> 17

<170> PatentIn version 3.1

<210> 1

<211> 3885

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (161)..(1705)

<223>

<220>

<221> misc\_feature

<222> (2487)..(2487)

<223> n is a, c, g or t.

<220>

<221> misc\_feature

<222> (2788)..(2788)

<223> n is a, c, g or t.

<400> 1

```

ccgggagggg ggagcggcgt tggaggccac cgtttccagc atcaacaaca gcaacttggtg      60
attggcgggtg accggatatt cagttgcaca tccccacatc aatgcactgc caatgggtta      120
tatcctgtgt tgtgacctca tggtttaagt gggaataaag atg agt ata agc agt      175
                                         Met Ser Ile Ser Ser
                                         1           5

gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt      223
Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe
                    10           15           20

tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc      271
Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser
                    25           30           35

aat ata aat ggt gcc ctc gtc cca ccc gct gca ttg att tct atc atc      319
Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile

```

40					45					50						
cag	aaa	ggt	cta	cag	tat	gta	gaa	gca	gaa	gtt	agt	att	aat	gag	gat	367
Gln	Lys	Gly	Leu	Gln	Tyr	Val	Glu	Ala	Glu	Val	Ser	Ile	Asn	Glu	Asp	
	55					60					65					
ggt	acc	ttg	ttt	gat	ggt	cga	cca	ata	gag	tct	ctg	tcc	ctg	ata	gat	415
Gly	Thr	Leu	Phe	Asp	Gly	Arg	Pro	Ile	Glu	Ser	Leu	Ser	Leu	Ile	Asp	
70					75					80					85	
gcc	gta	atg	cct	gat	gta	gta	caa	aca	aga	caa	caa	gct	tat	aga	gat	463
Ala	Val	Met	Pro	Asp	Val	Val	Gln	Thr	Arg	Gln	Gln	Ala	Tyr	Arg	Asp	
				90					95					100		
aag	ctt	gca	cag	caa	cag	gca	gca	gct	gct	gca	gct	gcc	gca	gct	gca	511
Lys	Leu	Ala	Gln	Gln	Gln	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	
			105					110					115			
gcc	agc	caa	caa	gga	tct	gca	aaa	aat	gga	gaa	aac	aca	gca	aat	ggg	559
Ala	Ser	Gln	Gln	Gly	Ser	Ala	Lys	Asn	Gly	Glu	Asn	Thr	Ala	Asn	Gly	
		120					125					130				
gag	gag	aat	gga	gca	cat	act	ata	gca	aat	aat	cat	act	gat	atg	atg	607
Glu	Glu	Asn	Gly	Ala	His	Thr	Ile	Ala	Asn	Asn	His	Thr	Asp	Met	Met	
	135					140					145					
gaa	gtg	gat	ggg	gat	gtt	gaa	atc	cct	cct	aat	aaa	gct	gtt	gtg	ttg	655
Glu	Val	Asp	Gly	Asp	Val	Glu	Ile	Pro	Pro	Asn	Lys	Ala	Val	Val	Leu	
150					155					160					165	
cgg	ggc	cat	gaa	tct	gaa	gtt	ttt	atc	tgt	gcc	tggt	aac	cct	gtt	agt	703
Arg	Gly	His	Glu	Ser	Glu	Val	Phe	Ile	Cys	Ala	Trp	Asn	Pro	Val	Ser	
				170					175					180		
gat	ctc	cta	gca	tca	ggg	tct	gga	gac	tca	aca	gca	aga	ata	tggt	aat	751
Asp	Leu	Leu	Ala	Ser	Gly	Ser	Gly	Asp	Ser	Thr	Ala	Arg	Ile	Trp	Asn	
			185					190					195			
ctt	agt	gag	aac	agc	acc	agt	ggc	tct	aca	cag	tta	gta	ctt	aga	cat	799
Leu	Ser	Glu	Asn	Ser	Thr	Ser	Gly	Ser	Thr	Gln	Leu	Val	Leu	Arg	His	
		200				205						210				
tgt	ata	cga	gaa	gga	ggg	caa	gat	gtt	ccg	agc	aac	aag	gat	gtc	aca	847
Cys	Ile	Arg	Glu	Gly	Gly	Gln	Asp	Val	Pro	Ser	Asn	Lys	Asp	Val	Thr	
	215					220					225					
tct	cta	gat	tggt	aat	agt	gaa	ggt	aca	ctt	cta	gca	act	ggt	tcc	tat	895
Ser	Leu	Asp	Trp	Asn	Ser	Glu	Gly	Thr	Leu	Leu	Ala	Thr	Gly	Ser	Tyr	
230					235					240					245	
gat	ggg	ttt	gcc	aga	ata	tggt	act	aaa	gat	ggt	aac	ctt	gct	agc	acc	943
Asp	Gly	Phe	Ala	Arg	Ile	Trp	Thr	Lys	Asp	Gly	Asn	Leu	Ala	Ser	Thr	
				250					255					260		
tta	ggg	cag	cat	aaa	ggc	cct	ata	ttt	gca	tta	aaa	tggt	aat	aag	aaa	991
Leu	Gly	Gln	His	Lys	Gly	Pro	Ile	Phe	Ala	Leu	Lys	Trp	Asn	Lys	Lys	
			265					270					275			
gga	aat	ttc	atc	cta	agt	gct	gga	gta	gac	aag	act	aca	att	att	tggt	1039
Gly	Asn	Phe	Ile	Leu	Ser	Ala	Gly	Val	Asp	Lys	Thr	Thr	Ile	Ile	Trp	
		280					285					290				
gac	gca	cat	act	ggt	gaa	gcc	aag	caa	cag	ttt	cct	ttt	cat	tca	gca	1087

09087701-11501

Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe Pro Phe His Ser Ala  
 295 300 305  
 cca gca ttg gat gtt gat tgg cag agc aac aac acc ttt gct tct tgt 1135  
 Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn Thr Phe Ala Ser Cys  
 310 315 320 325  
 agt aca gat atg tgc att cat gtc tgt aaa tta gga caa gac aga cct 1183  
 Ser Thr Asp Met Cys Ile His Val Cys Lys Leu Gly Gln Asp Arg Pro  
 330 335 340  
 att aaa aca ttc caa gga cat acg aat gaa gta aat gct atc aaa tgg 1231  
 Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val Asn Ala Ile Lys Trp  
 345 350 355  
 gac cca act ggc aat ctc ttg gcc tcc tgt tct gac gac atg act tta 1279  
 Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu  
 360 365 370  
 aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa 1327  
 Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln  
 375 380 385  
 cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg 1375  
 His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly  
 390 395 400 405  
 act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat 1423  
 Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp  
 410 415 420  
 tct act gtt agg tta tgg gat gta gac cga ggg ata tgc atc cat acc 1471  
 Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr  
 425 430 435  
 ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat 1519  
 Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp  
 440 445 450  
 ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg 1567  
 Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp  
 455 460 465  
 aac acg cag aca ggt gct cta gtt cac agc tat agg gga aca ggt gga 1615  
 Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr Arg Gly Thr Gly Gly  
 470 475 480 485  
 ata ttt gaa gtt tgc tgg aat gca gca gga gac aaa gtt gga gcc agt 1663  
 Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp Lys Val Gly Ala Ser  
 490 495 500  
 gca tca gat ggt tca gtt tgt gta tta gac ctt cgg aaa tag 1705  
 Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu Arg Lys  
 505 510  
 cgctactagt tggaagccat ggacogacta tgaatgtgta catagccaaa atgagtgtcc 1765  
 ctgacccatg taatgttata gtccacttg aaccatggcc agtccaatac agccaaatct 1825  
 aaaagaaata tatacataca gtgtatataa acaaaattac accctgaaga tgacagagtt 1885  
 ttgtcacagc ttgtgaattc tgttcaccaa gtgctggaat ctaatctgct gtgccccctaa 1945

0598701-1501  
 POST = 10/2/85

aatagcattt	agaagttttg	gatatgaaaa	acagaagaga	gaaaatatac	attataaaaag	2005
cagtacatac	atgtaccagt	ttttggatac	taaatgacag	ccttgtttct	cccctttgaa	2065
tcagcagaca	ccatggatta	tattcttttt	ttcccttcag	tagtgagcag	tttgtatgta	2125
cagagaaaat	ggacttacaa	aaacttgcag	cagtagtttg	ttcttgcttt	aaaatttcgt	2185
ttttggttta	gattatggat	gcatgaagta	agggagtga	tcagtttctt	gtttatatatt	2245
ttttcacctt	ttaaacaaaa	aattctttta	aatattttta	tgcattcttt	tgaagaggta	2305
gatgttttgt	acatttttat	gctcccagag	catatattca	gttggtgcat	gttgtggaag	2365
ggggaattgg	aaattaaaat	gaaaacctat	gactttggtc	ctgtcaatct	gtaagacaca	2425
tcagtaaaaa	ggtattatgc	tctgttggtt	ttgttttttt	gttttgcttt	tttttttttt	2485
tncttttttg	tttttttgtg	atgtggctta	aatgcaatag	tttctttttt	gggacatatt	2545
tctgccatt	aaagactaga	agggcacaa	ttttttttta	attaccatag	agaagataca	2605
ttaaaaaaaa	tcttctgatg	ttttgtagcc	ataactaaat	tatggtaaaa	atgtgcacta	2665
ttgtgaaaag	gagcaacgta	gttttggtt	ttttgttgtt	tgtttgtttt	gctttgtttt	2725
ttaagagatt	aaaatgtttc	tggataagga	ttagcttctc	gaagtgtcca	tcattctgtg	2785
tanaagctta	aatatgtaat	gtaaccaa	tccagtatta	aaaatctctc	atgttgtttt	2845
ctttatacaa	agcaagataa	cggcatataa	cactgccatt	acatggcaaa	atgtttgcta	2905
ccttagttta	aaaaacaatc	tcaaacaaaa	gacttgcttc	aagggtgttt	taaatagcag	2965
tgattcagaa	ttttttttta	tgaaagtata	attgcactaa	ccttcttctc	gctgctctga	3025
ttctgcattt	gtggtacttg	tgactacgtt	ttttcaaata	tagatagatt	taagctgcta	3085
attttttttt	tttttagta	at	cactactata	tcatgtcttt	tactctgttt	3145
gtattttctt	aaagatatag	atattaaacc	ttgtgctcat	gcaacttaga	gtaacatata	3205
cagacaaaatg	attgcatgag	gccatgttta	tatgtgtgac	taataaggct	tgcatgatt	3265
aacataatcc	aggtatgtca	tttctgaaga	gaatagtc	caaatttata	tctcgaagat	3325
tttaattaag	ggaattgctt	attgtttgag	cttagcaaat	taataacact	atctctgtca	3385
ctaattat	tt	tgaggccttt	tagtactaaa	attttaacct	gtgttctaag	3445
tttaacccaa	gtaatgcagc	tttgattgat	ttcagcattc	gttgctttgc	tatttttaca	3505
aaacagcatt	gattgaagca	agttttgggt	ttactaagg	agggtagcat	ttgctattgg	3565
taaagagaat	aaatacactt	aatttcacaa	tacattgtta	tatgtacccc	agttgttggt	3625
agtggggact	atgatactgt	aataatattt	ttaaaaattt	acatcaagag	aggcagtc	3685
tcacgatgg	tttgtgccag	ctcttttttag	ggttttggat	cacattagag	atatttagaa	3745
catattaccc	tgtgacttac	gtaggaaacc	taatatgctg	agtatctggc	acttgaattc	3805
ctgcttttat	tgctggagg	ccacatgtgt	ggttgacctc	tgttattggt	taaaaaaaaa	3865

090701 1150

aaaaaaaaaa aaaaaaaaaa

3885

<210> 2  
 <211> 514  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <400> 2

Met Ser Ile Ser Ser Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu  
 1 5 10 15

Gln Glu Ser Gly Phe Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser  
 20 25 30

His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala  
 35 40 45

Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val  
 50 55 60

Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser  
 65 70 75 80

Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln  
 85 90 95

Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala  
 100 105 110

Ala Ala Ala Ala Ala Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu  
 115 120 125

Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn  
 130 135 140

His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn  
 145 150 155 160

Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala  
 165 170 175

Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr  
 180 185 190

Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln  
 195 200 205

0998701-11501  
 FOSTT "T048880



Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr  
465 470 475 480

Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp  
485 490 495

Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu  
500 505 510

Arg Lys

<210> 3  
<211> 2078  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (161)..(1705)  
<223>

<400> 3  
ccgggagggg ggagcggcgt tggaggccac cgtttccagc atcaacaaca gcaacttggtg 60  
attggcgggtg accggatatt cagttgcaca tccccacatc aatgcactgc caatgggtta 120  
tattcctgtgt tgtgacctca tggtttaagt gggaataaag atg agt ata agc agt 175  
Met Ser Ile Ser Ser  
1 5  
gat gag gtc aac ttc ttg gta tat aga tac ttg caa gag tca gga ttt 223  
Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu Gln Glu Ser Gly Phe  
10 15 20  
tct cat tca gca ttt acc ttt ggt ata aaa agc cat atc agt cag tcc 271  
Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser His Ile Ser Gln Ser  
25 30 35  
aat ata aat ggt gcc ctg gtc cca ccc gct gca ttg att tct atc atc 319  
Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala Leu Ile Ser Ile Ile  
40 45 50  
cag aaa ggt cta cag tat gta gaa gca gaa gtt agt att aat gag gat 367  
Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val Ser Ile Asn Glu Asp  
55 60 65  
ggt acc ttg ttt gat ggt cga cca ata gag tct ctg tcc ctg ata gat 415  
Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser Leu Ser Leu Ile Asp  
70 75 80 85  
gcc gta atg cct gat gta gta caa aca aga caa caa gct tat aga gat 463  
Ala Val Met Pro Asp Val Val Gln Thr Arg Gln Gln Ala Tyr Arg Asp  
90 95 100  
aag ctt gca cag caa cag gca gca gct gct gca gct gcc gca gct gca 511

Page 8



gac cca act ggc aat ctc ttg gcc tcc tgt tct gac gac atg act tta 1279  
 Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser Asp Asp Met Thr Leu  
 360 365 370  
 aag ata tgg agt atg aaa caa gac aat tgt gtc cat gat ttg cag caa 1327  
 Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val His Asp Leu Gln Gln  
 375 380 385  
 cat aat aaa gaa att tat act atc aaa tgg agt cca aca gga cca ggg 1375  
 His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser Pro Thr Gly Pro Gly  
 390 395 400 405  
 act aat aat cca aat gcc aac ctt atg tta gca agt gca tcc ttt gat 1423  
 Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala Ser Ala Ser Phe Asp  
 410 415 420  
 tct act gtt agg tta tgg gat gta gac cga ggg ata tgc atc cat acc 1471  
 Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly Ile Cys Ile His Thr  
 425 430 435  
 ttg aca aaa cac caa gag cct gtg tac agt gta gct ttc agt cct gat 1519  
 Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val Ala Phe Ser Pro Asp  
 440 445 450  
 ggc agg tat ctg gca agt ggt tct ttt gac aaa tgt gta cac atc tgg 1567  
 Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys Cys Val His Ile Trp  
 455 460 465  
 aac acg cag gta tgt ctt cat tat tta aat ggt caa gtg ctc tta aat 1615  
 Asn Thr Gln Val Cys Leu His Tyr Leu Asn Gly Gln Val Leu Leu Asn  
 470 475 480 485  
 tta ggt aga agc att tgc cta tac act ctg cct cac cat ttg gtt gtc 1663  
 Leu Gly Arg Ser Ile Cys Leu Tyr Thr Leu Pro His His Leu Val Val  
 490 495 500  
 att cct ctt gtg gca tta att gaa tta ttg gtt tta aaa taa 1705  
 Ile Pro Leu Val Ala Leu Ile Glu Leu Leu Val Leu Lys  
 505 510  
 gatagaaact aatggaagtt atatctttat ggagactgga attttgaaat ggattttgat 1765  
 catttgttttt attattttatt attgtattct tttgtttttt tccaacgggt ttgcagatat 1825  
 cagatgtgaa tgtttaagat gtattttattt agataaatga cagattttat ttttcaaaat 1885  
 agttgtctcc gaaggagcta tatgtgagca gtaaaagtca aaggaccaga ttttatggct 1945  
 gaatgcaata atttatgaga aagaaactta caactacatt accttttcag gtaagtatgt 2005  
 atggtgtttc aaagattctt agaagtggag aaaacagtct ggtgctttca attttttaaa 2065  
 tcttctcaat ggt 2078  
 <210> 4  
 <211> 514  
 <212> PRT  
 <213> Homo sapiens  
 <400> 4  
 Met Ser Ile Ser Ser Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu

```

1           5           10           15

Gln Glu Ser Gly Phe Ser His Ser Ala Phe Thr Phe Gly Ile Lys Ser
      20              25              30

His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
      35              40              45

Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val
      50              55              60

Ser Ile Asn Glu Asp Gly Thr Leu Phe Asp Gly Arg Pro Ile Glu Ser
      65              70              75              80

Leu Ser Leu Ile Asp Ala Val Met Pro Asp Val Val Gln Thr Arg Gln
      85              90              95

Gln Ala Tyr Arg Asp Lys Leu Ala Gln Gln Gln Ala Ala Ala Ala Ala
      100             105             110

Ala Ala Ala Ala Ala Ala Ser Gln Gln Gly Ser Ala Lys Asn Gly Glu
      115             120             125

Asn Thr Ala Asn Gly Glu Glu Asn Gly Ala His Thr Ile Ala Asn Asn
      130             135             140

His Thr Asp Met Met Glu Val Asp Gly Asp Val Glu Ile Pro Pro Asn
      145             150             155             160

Lys Ala Val Val Leu Arg Gly His Glu Ser Glu Val Phe Ile Cys Ala
      165             170             175

Trp Asn Pro Val Ser Asp Leu Leu Ala Ser Gly Ser Gly Asp Ser Thr
      180             185             190

Ala Arg Ile Trp Asn Leu Ser Glu Asn Ser Thr Ser Gly Ser Thr Gln
      195             200             205

Leu Val Leu Arg His Cys Ile Arg Glu Gly Gly Gln Asp Val Pro Ser
      210             215             220

Asn Lys Asp Val Thr Ser Leu Asp Trp Asn Ser Glu Gly Thr Leu Leu
      225             230             235             240

Ala Thr Gly Ser Tyr Asp Gly Phe Ala Arg Ile Trp Thr Lys Asp Gly
      245             250             255

```

09570403550



<210>	5
<211>	20
<212>	DNA
<213>	Artificial Sequence

```
<400> 5
agggaatgta acccttctca 20
```

<210>	6
<211>	20
<212>	DNA
<213>	Artificial Sequence

```
<400> 6
tcttactaga tgcagtgacc 20
```

<210>	7
<211>	21
<212>	DNA
<213>	Artificial Sequence

<400> 7  
gatgagtata agcagtgatg t 21

<210>	8
<211>	29
<212>	DNA
<213>	Artificial Sequence

<400> 8  
ctatattttgt tctttccgaa ggtctaata 29

<210>	9
<211>	21
<212>	DNA
<213>	Artificial Sequence

```
<400> 9
caacagagct tcactttacc c
```

[illegible]

Page 14

```

365          370          375          380
gat aac tgt gtc cat gat ttg caa gca cat aat aaa gaa att tat act 1384
Asp Asn Cys Val His Asp Leu Gln Ala His Asn Lys Glu Ile Tyr Thr
          385          390          395

att aag tgg agt cca aca gga cca ggg aca aat aat cca aat gcc aac 1432
Ile Lys Trp Ser Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn
          400          405          410

ctt atg cta gca agt gca tcc ttt gat tct aca gtt agg tta tgg gac 1480
Leu Met Leu Ala Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp
          415          420          425

gta gac aga ggg att tgc atc cat act ttg aca aaa cat caa gag ccc 1528
Val Asp Arg Gly Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro
          430          435          440

gtg tac agt gtg gct ttt agt cct gat ggc agg tat ctg gca agt ggt 1576
Val Tyr Ser Val Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly
          445          450          455

tct ttt gac aag tgt gtg cac atc tgg aac aca cag aca ggt gct cta 1624
Ser Phe Asp Lys Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu
          465          470          475

gtt cac agt tac agg gga aca ggt gga att ttt gaa gtt tgc tgg aac 1672
Val His Ser Tyr Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn
          480          485          490

gca gca gga gac aaa gtt gga gcc agt gct tcg gac ggt tca gtt tgt 1720
Ala Ala Gly Asp Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys
          495          500          505

gtc tta gac ctt cgg aaa tag cgttactagt tggaagccat ggaccgacta 1771
Val Leu Asp Leu Arg Lys
          510

tgaatgtgta catagccaca agactatccc tgacccatat actgctatag tcccacttga 1831

accatggcca gtccactaca gc 1853

```

```

<210> 12
<211> 514
<212> PRT
<213> Mus musculus

```

```
<400> 12
```

```
Met Ser Ile Ser Ser Asp Glu Val Asn Phe Leu Val Tyr Arg Tyr Leu
1          5          10          15

```

```
Gln Glu Ser Gly Phe Ser His Ser Ala Phe Thr Phe Gly Ile Glu Ser
20          25          30

```

```
His Ile Ser Gln Ser Asn Ile Asn Gly Ala Leu Val Pro Pro Ala Ala
35          40          45

```

```
Leu Ile Ser Ile Ile Gln Lys Gly Leu Gln Tyr Val Glu Ala Glu Val

```

60

Thr Thr Ile Ile Trp Asp Ala His Thr Gly Glu Ala Lys Gln Gln Phe  
290 295 300



Pro Phe His Ser Ala Pro Ala Leu Asp Val Asp Trp Gln Ser Asn Asn  
305 310 315 320

Thr Phe Ala Ser Cys Ser Thr Asp Met Cys Ile His Val Cys Lys Leu  
325 330 335

Gly Gln Asp Arg Pro Ile Lys Thr Phe Gln Gly His Thr Asn Glu Val  
340 345 350

Asn Ala Ile Lys Trp Asp Pro Thr Gly Asn Leu Leu Ala Ser Cys Ser  
355 360 365

Asp Asp Met Thr Leu Lys Ile Trp Ser Met Lys Gln Asp Asn Cys Val  
370 375 380

His Asp Leu Gln Ala His Asn Lys Glu Ile Tyr Thr Ile Lys Trp Ser  
385 390 395 400

Pro Thr Gly Pro Gly Thr Asn Asn Pro Asn Ala Asn Leu Met Leu Ala  
405 410 415

Ser Ala Ser Phe Asp Ser Thr Val Arg Leu Trp Asp Val Asp Arg Gly  
420 425 430

Ile Cys Ile His Thr Leu Thr Lys His Gln Glu Pro Val Tyr Ser Val  
435 440 445

Ala Phe Ser Pro Asp Gly Arg Tyr Leu Ala Ser Gly Ser Phe Asp Lys  
450 455 460

Cys Val His Ile Trp Asn Thr Gln Thr Gly Ala Leu Val His Ser Tyr  
465 470 475 480

Arg Gly Thr Gly Gly Ile Phe Glu Val Cys Trp Asn Ala Ala Gly Asp  
485 490 495

Lys Val Gly Ala Ser Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu  
500 505 510

Arg Lys

<210> 13  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Synthetic

&lt;400&gt; 13

Cys Gly Val Ser His Gln Asn Pro Ser Lys  
 1 5 10

&lt;210&gt; 14

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 14

caagcttata gagataagct tgca

24

&lt;210&gt; 15

&lt;211&gt; 24

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 15

caggcttata gagataaact tgca

24

&lt;210&gt; 16

&lt;211&gt; 22

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 16

gtaagactct ccaactccca at

22

&lt;210&gt; 17

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic

&lt;400&gt; 17

Thr Gln Thr Gly Ala Leu Val His Ser Tyr Arg Gly Thr Gly Gly Ile  
 1 5 10 15

Phe Glu Val Cys Trp Asn Ala Cys Ala Gly Asp Lys Val Gly Ala Ser  
 20 25 30

Ala Ser Asp Gly Ser Val Cys Val Leu Asp Leu Arg  
 35 40